

# REPLACEMENT SHEET

Figure 1



10 20 30 40 50 60  
5' ACCATTGCTTTGGTTCCTTGGCAAACGAAAGTTTAGAACGAAACTGACCCAAATTACA  
70 80 90 100 110 120  
TCTTCCTCCTGGATCCTTACCATGGCTGGTTTGGTTGAAAGAAAGTATGCGCATCAAGATG  
M A G L L K E S M R I K M  
130 140 150 160 170 180  
TACATGGAAGGCACGGTTAATGGCCATTATTTCAGTGTGAAGGAGAGGGAGACGGCAAC  
Y M E G T V N G H Y F K C E G E G D G N  
190 200 210 220 230 240  
CCATTTACAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATT  
P F T G T Q S M R I H V T E G A P L P F  
250 260 270 280 290 300  
GCCTTCGACATTTTGGCACCGTGTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACG  
A F D I L A P C C E Y G S R T F V H H T  
310 320 330 340 350 360  
GCAGAGATTTCCCGATTTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACC  
A E I P D F F K Q S F P E G F T W E R T  
370 380 390 400 410 420  
ACAACCTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAAC  
T T Y E D G G I L T A H Q D T S L E G N  
430 440 450 460 470 480  
TGCCTTATATACAAGGTGAAAGTCCTTGGTACCAATTTTCTGCTGATGGCCCCGTGATG  
C L I Y K V K V L G T N F P A D G P V M  
490 500 510 520 530 540  
AAGAACAAATCAGGAGGATGGGAGCCATGCACTGAGGTGGTTTATCCAGAGAATGGTGT  
K N K S G G W E P C T E V V Y P E N G V  
550 560 570 580 590 600  
CTGTGTGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCTC  
L C G R N V M A L K V G D R R L I C H L  
610 620 630 640 650 660  
TATACTTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTTCAATTT  
Y T S Y R S K K A V R A L T M P G F H F  
670 680 690 700 710 720  
ACAGACATCCGCCTTCAGATGCCGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAA  
T D I R L Q M P R K K K D E Y F E L Y E  
730 740 750 760 770 780  
GCATCTGTGGCTAGGTACAGTGATCTTCTTGAAAAAGCAAATTGATTGTTCCCAAGTGACA  
A S V A R Y S D L P E K A N \*  
790 800 810 820 830 840  
CCAGACTGCTGTCAGCTTTTGGTTAAAGCCCCGAAAGACAAAAGGACATTTGTAGTTTAGT  
850 860 870 880 890 900  
TTATATTTCCCTTTTCATTTGTGAATCAACATTGTACTCTCTGTAAACCTTTAAAATGCTC  
910  
CATTAACCT 3' (SEQ ID Nos: 01 & 02)

## REPLACEMENT SHEET

Figure 2

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      10      20      30      40      50      60
5' ACCATTGCTTTGGTTCCTTGGCAAACGAAAGTTTAGACGAAAAGTACCCAAATTACAT

      70      80      90     100     110     120
CCTCCTGATCCTTACCATGGCTGGTTTGTGAAAGAAAGTATGCGCATCAAGATGTACAT
      M A G L L K E S M R I K M Y M

      130     140     150     160     170     180
GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT
      E G T V N G H Y F K C E G E G D G N P F

      190     200     210     220     230     240
TACAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTGCCTT
      T G T Q S M R I H V T E G A P L P F A F

      250     260     270     280     290     300
CGACATTTTGGCACCGTGTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGA
      D I L A P C C E Y G S R T F V H H T A E

      310     320     330     340     350     360
GATTCCCGATTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACCACAAC
      I P D F F K Q S F P E G F T W E R T T T

      370     380     390     400     410     420
CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAACTGCCT
      Y E D G G I L T A H Q D T S L E G N C L

      430     440     450     460     470     480
TATATACAAGGTGAAAGTCCTTGGTACCAATTTTCTGCTGATGGCCCCGTGATGAAGAA
      I Y K V K V L G T N F P A D G P V M K N

      490     500     510     520     530     540
CAAATCAGAAGGATGGGAGCCATGCACTGAGGTGGTTTATCCAGATAATGGTGTCTCTGTG
      K S E G W E P C T E V V Y P D N G V L C

      550     560     570     580     590     600
TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCTCTATAC
      G R N V M A L K V G D R R L I C H L Y T

      610     620     630     640     650     660
TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTTCAATTTACAGA
      S Y R S K K A V R A L T M P G F H F T D

      670     680     690     700     710     720
CATCCGCCTTCAGATGCCGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAAGCATC
      I R L Q M P R K K K D E Y F E L Y E A S

      730     740     750     760     770     780
TGTGGCTAGGTACAGTGATCTTCTGAAAAAGCAAATTGATTGTTCCCAGTGACACCAGA
      V A R Y S D L P E K A N *

      790     800     810     820     830     840
CTGCTGTCAGCTTTTGGTTAAAGCCCCGAAAGACAAAAGGACATTTGTAGTTTTAGTTTAT

      850     860     870     880     890     900
ATTTTCCCTTTCATTTTGTGAATCAACATTGTACTCTCTGTAAACCTTTAAAATGCTCCA

TTAAACCT 3' (SEQ ID NOS: 03 & 04)
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## REPLACEMENT SHEET

Figure 4

ATGGCTGGTTTGTGAAAGAAAGTATGCGCATCAAGATG  
M A G L L K E S M R I K M

TACATGGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAAC  
Y M E G T V N G H Y F K C E G E G D G N

CCATTTACAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTT  
P F T G T Q S M R I H V T E G A P L P F

GCCTTCGACATTTTGGCACCGTGTTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACG  
A F D I L A P C C E Y G S R T F V H H T

GCAGAGATTCCCGATTTCTTCAAGCAGTCTTCCCTGAAGGCTTTACTTGGGAAAGAACC  
A E I P D F F K Q S F P E G F T W E R T

ACAACCTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAAC  
T T Y E D G G I L T A H Q D T S L E G N

TGCCTTATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATG  
C L I Y K V K V L G T N F P A D G P V M

AAGAACAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTG  
K N K S G G W E P S T E V V Y P E N G V

CTGTGTGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCTC  
L C G R N V M A L K V G D R R L I C H L

TATACTTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTTCAATTT  
Y T S Y R S K K A V R A L T M P G F H F

ACAGACATCCGCCTTCAGATGCCGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAA  
T D I R L Q M P R K K K D E Y F E L Y E

GCATCTGTGGCTAGGTACAGTGATCTTCTGAAAAAGCAAATTGA  
A S V A R Y S D L P E K A N \*

(SEQ ID NOS: 05 & 06)

# REPLACEMENT SHEET

Figure 6

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      80      90      100      110      120
      ATGTCTGGTTTGTGAAAGAAAGTATGCGCATCAAGATGTACAT
      M S G L L K E S M R I K M Y M

      130      140      150      160      170      180
      GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT
      E G T V N G H Y F K C E G E G D G N P F

      190      200      210      220      230      240
      TGCAGGTACGCAGAGCATGAGGATTCATGTACCGAAGGGGCTCCATTACCATTTCCTT
      A G T Q S M R I H V T E G A P L P F A F

      250      260      270      280      290      300
      CGACATTTTGGCACCGTGTGTGAGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGA
      D I L A P C C E Y G S R T F V H H T A E

      310      320      330      340      350      360
      GATTCCCGATTCTTCAAGCAGTCTTTCCTGAAGGCTTTACTTGGGAAAGAACCACAAC
      I P D F F K Q S F P E G F T W E R T T T

      370      380      390      400      410      420
      CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAAGTGCCT
      Y E D G G I L T A H Q D T S L E G N C L

      430      440      450      460      470      480
      TATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATGAAGAA
      I Y K V K V L G T N F P A D G P V M K N

      490      500      510      520      530      540
      CAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTCTCTGTG
      K S G G W E P S T E V V Y P E N G V L C

      550      560      570      580      590      600
      TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCACTATAC
      G R N V M A L K V G D R R L I C H H Y T

      610      620      630      640      650      660
      TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTTCATTTTACAGA
      S Y R S K K A V R A L T M P G F H F T D

      670      680      690      700      710      720
      CATCCGCCTTCAGATGCTGAGGAAAGAGAAAGACGAGTACTTTGAACTGTACGAAGCATC
      I R L Q M L R K E K D E Y F E L Y E A S

      730      740      750      760
      TGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGA
      V A R Y S D L P E K A N * (SEQ ID NOs: 07 & 08)
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## REPLACEMENT SHEET

Figure 8

ATGTCTGGTTTGTGAAAGAAAGTATGCGCATCAAGATGTACAT  
M S G L L K E S M R I K M Y M

GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT  
E G T V N G H Y F K C E G E G D G N P F

TGCAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTCCTT  
A G T Q S M R I H V T E G A P L P F A F

CGACATTTTGGCACCGTGTGTGCGTACGGCAGCAGGACCTTTGTCCACCATAACGGCAGA  
D I L A P C C A Y G S R T F V H H T A E

GATTCCCGATTCTTCAAGCAGTCTTTCCTGAAGGCTTTACTTGGGAAAGAACCACAAC  
I P D F F K Q S F P E G F T W E R T T T

CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAACTGCCT  
Y E D G G I L T A H Q D T S L E G N C L

←

TATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATGAAGAA  
I Y K V K V L G T N F P A D G P V M K N

CAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTCTCTGTG  
K S G G W E P S T E V V Y P E N G V L C

TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCACTATAC  
G R N V M A L K V G D R R L I C H H Y T

TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTTCATTTTACAGA  
S Y R S K K A V R A L T M P G F H F T D

CATCCGCCTTCAGATGCTGAGGAAAGAGAAAGACGAGTACTTTGAACTGTACGAAGCATC  
I R L Q M L R K E K D E Y F E L Y E A S

TGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGA  
V A R Y S D L P E K A N \*

(SEQ ID NO: 09 & 10)

## REPLACEMENT SHEET

Figure 10

A.

M S G L L K E S M R I K M Y M E G T V N G H Y  
F K C E G E G D G N P F A G T Q S M R I H V T  
E G A P L P F A F D I L A P C C E Y G S R T F  
V H H T A E I P D F F K Q S F P E G F T W E R  
T T T Y E D G G I L T A H Q D T S L E G N C L  
I Y K V K V H G T N F P A D G P V M K N K S G  
G W E P S T E V V Y P E N G V L C G R N V M A  
L K V G D R H L I C H H Y T S Y R S K K A V R  
A L T M P G F H F T D I R L Q M L R K K K D E  
Y F E L Y E A S V A R Y S D L P E K A N (SEQ ID  
NO:12)

B.

ATGGTGAGCGGCCTGCTGAAGGAGAGTATGCGCATCAAGATGTACATGGAGGGCACCGTGAACGGCCAC  
TACTTCAAGTGCGAGGGCGAGGGCGACGGCAACCCCTTCGCCGGCACCCAGAGCATGAGAATCCACGTG  
ACCGAGGGCGCCCCCTGCCCTTCGCCTTCGACATCCTGGCCCCCTGCTGCGAGTACGGCAGCAGGACC  
TTCGTGCACCACACCGCCGAGATCCCCGACTTCTTCAAGCAGAGCTTCCCCGAGGGCTTCACCTGGGAG  
AGAACCACCACCTACGAGGACGGCGGCATCCTGACCGCCCACCAGGACACCAGCCTGGAGGGCAACTGC  
CTGATCTACAAGGTGAAGGTGCACGGCACCAACTTCCCCGCCGACGGCCCCGTGATGAAGAACAAGAGC  
GGCGGCTGGGAGCCCAGCACCGAGGTGGTGTACCCCGAGAACGGCGTGCTGTGCGGCCGGAACGTGATG  
GCCCTGAAGGTGGGCGACCGGCACCTGATCTGCCACCACTACACCAGCTACCGGAGCAAGAAGGCCGTG  
CGCGCCCTGACCATGCCCCGCTTCCACTTCACCGACATCCGGCTCCAGATGCTGCGGAAGAAGAAGGAC  
GAGTACTTCGAGCTGTACGAGGCCAGCGTGGCCCGGTACAGCGACCTGCCCCGAGAAGGCCAACTGA  
(SEQ ID NO:11)

C.

MSGLLKESMRIKMYMEGTVNGHYFKCEGEDGNPFAGTQSMRIHVTEGAPLPFAFDILAPCCEYGSRTF  
VHHTAEIPDFFKQSFPEGFTWERTTTTYEDGGILTAAHQDTSLEGNCLIYKVKVHGNTNFPADGPVMKNKSG  
GWEPSTEVVYPENGVLCGRNVMALKVGDRLICHHYTSYRSKKAVRALTMPGFHFTDIRLQMLRKEKDE  
YFELYEASVARYSDLPEKAN\* SEQ ID NO:14)

D.

ATGGTGAGCGGCCTGCTGAAGGAGAGCATGCGCATCAAGATGTACATGGAGGGCACCGTGAACGGCCAC  
TACTTCAAGTGCGAGGGCGAGGGCGACGGCAACCCCTTCGCCGGCACCCAGAGCATGCGGATCCACGTG  
ACCGAGGGCGCCCCCTGCCCTTCGCCTTCGACATCCTGGCCCCCTGCTGCGAGTACGGCAGCAGGACC  
TTCGTGCACCACACCGCCGAGATCCCCGACTTCTTCAAGCAGAGCTTCCCCGAGGGCTTCACCTGGGAG  
AGAACCACCACCTACGAGGACGGCGGCATCCTGACCGCCCACCAGGACACCAGCCTGGAGGGCAACTGC  
CTGATCTACAAGGTGAAGGTGCTGGGCACCAACTTCCCCGCCGACGGCCCCGTGATGAAGAACAAGAGC  
GGCGGCTGGGAGCCCAGCACCGAGGTGGTGTACCCCGAGAACGGCGTGCTGTGCGGCCGGAACGTGATG  
GCCCTGAAGGTGGGCGACCGGCGGCTGATCTGCCACCACTACACCAGCTACCGGAGCAAGAAGGCCGTG  
CGGGCCCTGACCATGCCCCGCTTCCACTTCACCGACATCCGGCTGCAGATGCTGCGGAAGGAGAAGGAC  
GAGTACTTCGAGCTGTACGAGGCCAGCGTGGCCCGGTACAGCGACCTGCCCCGAGAAGGCCAACTGA  
(SEQ ID NO:13)

# REPLACEMENT SHEET

FIGURE 12

1	A	CCG	GTC	GCC	ACC	ATG	GTG	AGC	GGC	CTG	CTG	AAG	GAG	AGC	ATG	CGC	46
1	AgeI					M	V	S	G	L	L	K	E	S	M	R	11
47	ATC	AAG	ATG	TAC	ATG	GAG	GGC	ACC	GTG	AAC	GGC	CAC	TAC	TTC	AAG	TGC	94
12	I	K	M	Y	M	E	G	T	V	N	G	H	Y	F	K	C	27
95	GAG	GGC	GAG	GGC	GAC	GGC	AAC	CCC	TTC	GCC	GGC	ACC	CAG	AGC	ATG	CGG	142
28	E	G	E	G	D	G	N	P	F	A	G	T	Q	S	M	R	43
143	ATC	CAC	GTG	ACC	GAG	GGC	GCC	CCC	CTG	CCC	TTC	GCC	TTC	GAC	ATC	CTG	190
44	I	H	V	T	E	G	A	P	L	P	F	A	F	D	I	L	59
191	GCC	CCC	TGC	TGC	GAG	TAC	GGC	AGC	AGG	ACC	TTC	GTG	CAC	CAC	ACC	GCC	238
60	A	P	C	C	E	Y	G	S	R	T	F	V	H	H	T	A	75
239	GAG	ATC	CCC	GAC	TTC	TTC	AAG	CAG	AGC	TTC	CCC	GAG	GGC	TTC	ACC	TGG	286
76	E	I	P	D	F	F	K	Q	S	F	P	E	G	F	T	W	91
287	GAG	AGA	ACC	ACC	ACC	TAC	GAG	GAC	GGC	GGC	ATC	CTG	ACC	GCC	CAC	CAG	334
92	E	R	T	T	T	Y	E	D	G	G	I	L	T	A	H	Q	107
335	GAC	ACC	AGC	CTG	GAG	GGC	AAC	TGC	CTG	ATC	TAC	AAG	GTG	AAG	GTG	CTG	382
108	D	T	S	L	E	G	N	C	L	I	Y	K	V	K	V	L	123
383	GGC	ACC	AAC	TTC	CCC	GCC	GAC	GGC	CCC	GTG	ATG	AAG	AAC	AAG	AGC	GGC	430
124	G	T	N	F	P	A	D	G	P	V	M	K	N	K	S	G	139
431	GGC	TGG	GAG	CCC	AGC	ACC	GAG	GTG	GTG	TAC	CCC	GAG	AAC	GGC	GTG	CTG	478
140	G	W	E	P	S	T	E	V	V	Y	P	E	N	G	V	L	155
479	TGC	GGC	CGG	AAC	GTG	ATG	GCC	CTG	AAG	GTG	GGC	GAC	CGG	CGG	CTG	ATC	526
156	C	G	R	N	V	M	A	L	K	V	G	D	R	R	L	I	171
527	TGC	CAC	CAC	TAC	ACC	AGC	TAC	CGG	AGC	AAG	AAG	GCC	GTG	CGG	GCC	CTG	574
172	C	H	H	Y	T	S	Y	R	S	K	K	A	V	R	A	L	187
575	ACC	ATG	CCC	GGC	TTC	CAC	TTC	ACC	GAC	ATC	CGG	CTG	CAG	ATG	CTG	CGG	622
188	T	M	P	G	F	H	F	T	D	I	R	L	Q	M	L	R	203
623	AAG	GAG	AAG	GAC	GAG	TAC	TTC	GAG	CTG	TAC	GAG	GCC	AGC	GTG	GCC	CGG	670
204	K	E	K	D	E	Y	F	E	L	Y	E	A	S	V	A	R	219
671	TAC	AGC	GAC	CTG	CCC	GAG	AAG	GCC	AAC	<u>AGA TCT CCC GGG</u>	ATG	GTG	AGC				718
220	Y	S	D	L	P	E	K	A	N	R	S	P	G	M	V	S	235
719	GGC	CTG	CTG	AAG	GAG	AGC	ATG	CGC	ATC	AAG	ATG	TAC	ATG	GAG	GGC	ACC	766
236	G	L	L	K	E	S	M	R	I	K	M	Y	M	E	G	T	251
767	GTG	AAC	GGC	CAC	TAC	TTC	AAG	TGC	GAG	GGC	GAG	GGC	GAC	GGC	AAC	CCC	814
252	V	N	G	H	Y	F	K	C	E	G	E	G	D	G	N	P	267
815	TTC	GCC	GGC	ACC	CAG	AGC	ATG	CGG	ATC	CAC	GTG	ACC	GAG	GGC	GCC	CCC	862
268	F	A	G	T	Q	S	M	R	I	H	V	T	E	G	A	P	283
863	CTG	CCC	TTC	GCC	TTC	GAC	ATC	CTG	GCC	CCC	TGC	TGC	GAG	TAC	GGC	AGC	910
284	L	P	F	A	F	D	I	L	A	P	C	C	E	Y	G	S	299

# REPLACEMENT SHEET

Figure 12 (continued)

911	AGG	ACC	TTC	GTG	CAC	CAC	ACC	GCC	GAG	ATC	CCC	GAC	TTC	TTC	AAG	CAG	958	
300	R	T	F	V	H	H	T	A	E	I	P	D	F	F	K	Q	315	
959	AGC	TTC	CCC	GAG	GGC	TTC	ACC	TGG	GAG	AGA	ACC	ACC	ACC	TAC	GAG	GAC	1006	
316	S	F	P	E	G	F	T	W	E	R	T	T	T	Y	E	D	331	
1007	GGC	GGC	ATC	CTG	ACC	GCC	CAC	CAG	GAC	ACC	AGC	CTG	GAG	GGC	AAC	TGC	1054	
332	G	G	I	L	T	A	H	Q	D	T	S	L	E	G	N	C	347	
1055	CTG	ATC	TAC	AAG	GTG	AAG	GTG	CTG	GGC	ACC	AAC	TTC	CCC	GCC	GAC	GGC	1102	
348	L	I	Y	K	V	K	V	L	G	T	N	F	P	A	D	G	363	
1103	CCC	GTG	ATG	AAG	AAC	AAG	AGC	GGC	GGC	TGG	GAG	CCC	AGC	ACC	GAG	GTG	1150	
364	P	V	M	K	N	K	S	G	G	W	E	P	S	T	E	V	379	
1151	GTG	TAC	CCC	GAG	AAC	GGC	GTG	CTG	TGC	GGC	CGG	AAC	GTG	ATG	GCC	CTG	1198	
380	V	Y	P	E	N	G	V	L	C	G	R	N	V	M	A	L	395	
1199	AAG	GTG	GGC	GAC	CGG	CGG	CTG	ATC	TGC	CAC	CAC	TAC	ACC	AGC	TAC	CGG	1246	
396	K	V	G	D	R	R	L	I	C	H	H	Y	T	S	Y	R	411	
1247	AGC	AAG	AAG	GCC	GTG	CGG	GCC	CTG	ACC	ATG	CCC	GGC	TTC	CAC	TTC	ACC	1294	
412	S	K	K	A	V	R	A	L	T	M	P	G	F	H	F	T	427	
1295	GAC	ATC	CGG	CTG	CAG	ATG	CTG	CGG	AAG	GAG	AAG	GAC	GAG	TAC	TTC	GAG	1342	
428	D	I	R	L	Q	M	L	R	K	E	K	D	E	Y	F	E	443	
1343	CTG	TAC	GAG	GCC	AGC	GTG	GCC	CGG	TAC	AGC	GAC	CTG	CCC	GAG	AAG	GCC	1390	
444	L	Y	E	A	S	V	A	R	Y	S	D	L	P	E	K	A	459	
1391	AAC	TGA																
460	N	*																

(SEQ ID NOS. 15 & 16)



# REPLACEMENT SHEET

Figure 13

1	A	CCG	GTC	GCC	ACC	ATG	GTG	AGC	GGC	CTG	CTG	AAG	GAG	AGC	ATG	CGC	46
1	AgeI					M	V	S	G	L	L	K	E	S	M	R	11
47	ATC	AAG	ATG	TAC	ATG	GAG	GGC	ACC	GTG	AAC	GGC	CAC	TAC	TTC	AAG	TGC	94
12	I	K	M	Y	M	E	G	T	V	N	G	H	Y	F	K	C	27
95	GAG	GGC	GAG	GGC	GAC	GGC	AAC	CCC	TTC	GCC	GGC	ACC	CAG	AGC	ATG	CGG	142
28	E	G	E	G	D	G	N	P	F	A	G	T	Q	S	M	R	43
143	ATC	CAC	GTG	ACC	GAG	GGC	GCC	CCC	CTG	CCC	TTC	GCC	TTC	GAC	ATC	CTG	190
44	I	H	V	T	E	G	A	P	L	P	F	A	F	D	I	L	59
191	GCC	CCC	TGC	TGC	GAG	TAC	GGC	AGC	AGG	ACC	TTC	GTG	CAC	CAC	ACC	GCC	238
60	A	P	C	C	E	Y	G	S	R	T	F	V	H	H	T	A	75
239	GAG	ATC	CCC	GAC	TTC	TTC	AAG	CAG	AGC	TTC	CCC	GAG	GGC	TTC	ACC	TGG	286
76	E	I	P	D	F	F	K	Q	S	F	P	E	G	F	T	W	91
287	GAG	AGA	ACC	ACC	ACC	TAC	GAG	GAC	GGC	GGC	ATC	CTG	ACC	GCC	CAC	CAG	334
92	E	R	T	T	T	Y	E	D	G	G	I	L	T	A	H	Q	107
335	GAC	ACC	AGC	CTG	GAG	GGC	AAC	TGC	CTG	ATC	TAC	AAG	GTG	AAG	GTG	CTG	382
108	D	T	S	L	E	G	N	C	L	I	Y	K	V	K	V	L	123
383	GGC	ACC	AAC	TTC	CCC	GCC	GAC	GGC	CCC	GTG	ATG	AAG	AAC	AAG	AGC	GGC	430
124	G	T	N	F	P	A	D	G	P	V	M	K	N	K	S	G	139
431	GGC	TGG	GAG	CCC	AGC	ACC	GAG	GTG	GTG	TAC	CCC	GAG	AAC	GGC	GTG	CTG	478
140	G	W	E	P	S	T	E	V	V	Y	P	E	N	G	V	L	155
479	TGC	GGC	CGG	AAC	GTG	ATG	GCC	CTG	AAG	GTG	GGC	GAC	CGG	CGG	CTG	ATC	526
156	C	G	R	N	V	M	A	L	K	V	G	D	R	R	L	I	171
527	TGC	CAC	CAC	TAC	ACC	AGC	TAC	CGG	AGC	AAG	AAG	GCC	GTG	CGG	GCC	CTG	574
172	C	H	H	Y	T	S	Y	R	S	K	K	A	V	R	A	L	187
575	ACC	ATG	CCC	GGC	TTC	CAC	TTC	ACC	GAC	ATC	CGG	CTG	CAG	ATG	CTG	CGG	622
188	T	M	P	G	F	H	F	T	D	I	R	L	Q	M	L	R	203
623	AAG	GAG	AAG	GAC	GAG	TAC	TTC	GAG	CTG	TAC	GAG	GCC	AGC	GTG	GCC	CGG	670
204	K	E	K	D	E	Y	F	E	L	Y	E	A	S	V	A	R	219
671	TAC	AGC	GAC	CTG	CCC	GAG	AAG	GCC	AAC	<u>AGA TCT CCC GGG</u>	ATG	GTG	AGC				718
220	Y	S	D	L	P	E	K	A	N	<u>R S P G</u>							235
719	GGC	CTG	CTG	AAG	GAG	AGC	ATG	CGC	ATC	AAG	ATG	TAC	ATG	GAG	GGC	ACC	766
236	G	L	L	K	E	S	M	R	I	K	M	Y	M	E	G	T	251
767	GTG	AAC	GGC	CAC	TAC	TTC	AAG	TGC	GAG	GGC	GAG	GGC	GAC	GGC	AAC	CCC	814
252	V	N	G	H	Y	F	K	C	E	G	E	G	D	G	N	P	267
815	TTC	GCC	GGC	ACC	CAG	AGC	ATG	CGG	ATC	CAC	GTG	ACC	GAG	GGC	GCC	CCC	862
268	F	A	G	T	Q	S	M	R	I	H	V	T	E	G	A	P	283

# REPLACEMENT SHEET

Figure 13 (continued)

863	CTG	CCC	TTC	GCC	TTC	GAC	ATC	CTG	GCC	CCC	TGC	TGC	GAG	TAC	GGC	AGC	910
284	L	P	F	A	F	D	I	L	A	P	C	C	E	Y	G	S	299
911	AGG	ACC	TTC	GTG	CAC	CAC	ACC	GCC	GAG	ATC	CCC	GAC	TTC	TTC	AAG	CAG	958
300	R	T	F	V	H	H	T	A	E	I	P	D	F	F	K	Q	315
959	AGC	TTC	CCC	GAG	GGC	TTC	ACC	TGG	GAG	AGA	ACC	ACC	ACC	TAC	GAG	GAC	1006
316	S	F	P	E	G	F	T	W	E	R	T	T	T	Y	E	D	331
1007	GGC	GGC	ATC	CTG	ACC	GCC	CAC	CAG	GAC	ACC	AGC	CTG	GAG	GGC	AAC	TGC	1054
332	G	G	I	L	T	A	H	Q	D	T	S	L	E	G	N	C	347
1055	CTG	ATC	TAC	AAG	GTG	AAG	GTG	CTG	GGC	ACC	AAC	TTC	CCC	GCC	GAC	GGC	1102
348	L	I	Y	K	V	K	V	L	G	T	N	F	P	A	D	G	363
1103	CCC	GTG	ATG	AAG	AAC	AAG	AGC	GGC	GGC	TGG	GAG	CCC	AGC	ACC	GAG	GTG	1150
364	P	V	M	K	N	K	S	G	G	W	E	P	S	T	E	V	379
1151	GTG	TAC	CCC	GAG	AAC	GGC	GTG	CTG	TGC	GGC	CGG	AAC	GTG	ATG	GCC	CTG	1198
380	V	Y	P	E	N	G	V	L	C	G	R	N	V	M	A	L	395
1199	AAG	GTG	GGC	GAC	CGG	CGG	CTG	ATC	TGC	CAC	CAC	TAC	ACC	AGC	TAC	CGG	1246
396	K	V	G	D	R	R	L	I	C	H	H	Y	T	S	Y	R	411
1247	AGC	AAG	AAG	GCC	GTG	CGG	GCC	CTG	ACC	ATG	CCC	GGC	TTC	CAC	TTC	ACC	1294
412	S	K	K	A	V	R	A	L	T	M	P	G	F	H	F	T	427
1295	GAC	ATC	CGG	CTG	CAG	ATG	CTG	CGG	AAG	GAG	AAG	GAC	GAG	TAC	TTC	GAG	1342
428	D	I	R	L	Q	M	L	R	K	E	K	D	E	Y	F	E	443
1343	CTG	TAC	GAG	GCC	AGC	GTG	GCC	CGG	TAC	AGC	GAC	CTG	CCC	GAG	AAG	GCC	1390
444	L	Y	E	A	S	V	A	R	Y	S	D	L	P	E	K	A	459
1391	AAC	AGA	ACT	CGA	GCT	ATG	GAT	GAT	GAT	ATC	GCC	G...					1424
460	N	R	T	R	A	M	D	D	D	I	A...						470

actin

(SEQ ID NOS. 17 & 18).

## REPLACEMENT SHEET

Figure 15

ATGGCTGGTTTGTGAAAGAAAGTATGCGCATCAAGATGTACAT  
M A G L L K E S M R I K M Y M

GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT  
E G T V N G H Y F K C E G E G D G N P F

TACAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTCCTT  
T G T Q S M R I H V T E G A P L P F A F

CGACATTTTGGCACCGTGTGTGAGTACGGCAGCAGGACCTTTGTCCACCATAACGGCAGA  
D I L A P C C E Y G S R T F V H H T A E

GATTCCCATTCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACCACAAC  
I P D F F K Q S F P E G F T W E R T T T

CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAACTGCCT  
Y E D G G I L T A H Q D T S L E G N C L

TATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATGAAGAA  
I Y K V K V L G T N F P A D G P V M K N

CAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTCTGTG  
K S G G W E P S T E V V Y P E N G V L C

TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCTCTATAC  
G R N V M A L K V G D R R L I C H L Y T

TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTCATTTTACAGA  
S Y R S K K A V R A L T M P G F H F T D

CATCCGCCTTCAGATGCCGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAAGCATC  
I R L Q M P R K K K D E Y F E L Y E A S

TGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGA  
V A R Y S D L P E K A N \*

SEQ ID NO:23 & 24

# REPLACEMENT SHEET

Figure 16

ATGTCTGGTTTGTGAAAGAAAGTATGCGCATCAAGATGTACAT  
M S G L L K E S M R I K M Y M

GGAAGGCACGGTTAATGGCCATTATTTCAAGTGTGAAGGAGAGGGAGACGGCAACCCATT  
E G T V N G H Y F K C E G E G D G N P F

TGCAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTTCCTT  
A G T Q S M R I H V T E G A P L P F A F

CGACATTTTGGCACCGTGTGTGCGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGA  
D I L A P C C A Y G S R T F V H H T A E

GATTCCCGATTTCCTTCAAGCAGTCTTTCCCTGAAGGCTTTACTTTGGGAAAGAACCACAAC  
I P D F F K Q S F P E G F T W E R T T T

CTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAAGTGCCT  
Y E D G G I L T A H Q D T S L E G N C L

←

TATATACAAGGTGAAAGTCCTTGGTACCAATTTTCCTGCTGATGGCCCCGTGATGAAGAA  
I Y K V K V L G T N F P A D G P V M K N

CAAATCAGGAGGATGGGAGCCAAGCACTGAGGTGGTTTATCCAGAGAATGGTGTCTCTGTG  
K S G G W E P S T E V V Y P E N G V L C

TGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCACTATAC  
G R N V M A L K V G D R R L I C H H Y T

TTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTTATTTTACAGA  
S Y R S K K A V R A L T M P G F H F T D

CATCCGCCTTCAGATGCTGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAAGCATC  
I R L Q M L R K K K D E Y F E L Y E A S

TGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAATTGA  
V A R Y S D L P E K A N \*

SEQ ID NO:25 & 26

# REPLACEMENT SHEET

Figure 17

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      10      20      30      40      50      60
5' ACCATTGCTTTGGTTCCTTGGCAAACGAAAGTTTAGAACGAAACTGACCCAAATTACA
      70      80      90     100     110     120
TCTTCCTCCTGGATCCTTACCATGGCTGGTTTGTGAAAGAAAGTATGCGCATCAAGATG
      M A G L L K E S M R I K M
      130     140     150     160     170     180
TACATGGAAGGCACGGTTAATGGCCATTATTCAAGTGTGAAGGAGAGGGAGACGGCAAC
Y M E G T V N G H Y F K C E G E G D G N
      190     200     210     220     230     240
CCATTTACAGGTACGCAGAGCATGAGGATTCATGTCACCGAAGGGGCTCCATTACCATTT
P F T G T Q S M R I H V T E G A P L P F
      250     260     270     280     290     300
GCCTTCGACATTTTGGCACCGTGTGTGAGTACGGCAGCAGGACCTTGTCCACCATACG
A F D I L A P C C E Y G S R T F V H H T
      310     320     330     340     350     360
GCAGAGATTCCCGATTCTTCAAGCAGTCTTCCCTGAAGGCTTTACTTGGGAAAGAACC
A E I P D F F K Q S F P E G F T W E R T
      370     380     390     400     410     420
ACAACCTATGAAGATGGAGGCATTCTTACTGCTCATCAGGACACAAGCCTGGAGGGGAAC
T T Y E D G G I L T A H Q D T S L E G N
      430     440     450     460     470     480
TGCCTTATATACAAGGTGAAAGTCCTTGGTACCAATTTTCTGCTGATGGCCCCGTGATG
C L I Y K V K V L G T N F P A D G P V M
      490     500     510     520     530     540
AAGAACAAATCAGGAGGATGGGAGCCATGCACTGAGGTGGTTTATCCAGAGAATGGTGTG
K N K S G G W E P C T E V V Y P E N G V
      550     560     570     580     590     600
CTGTGTGGACGTAATGTGATGGCCCTTAAAGTCGGTGATCGTCGTTTGATCTGCCATCTC
L C G R N V M A L K V G D R R L I C H L
      610     620     630     640     650     660
TATACTTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTTATTTT
Y T S Y R S K K A V R A L T M P G F H F
      670     680     690     700     710     720
ACAGACATCCGCCTTCAGATGCCGAGGAAAACGAAAGACGAGTACTTTGAACTGTACGAA
T D I R L Q M P R K T K D E Y F E L Y E
      730     740     750     760     770     780
GCATCTGTGGCTAGGTACAGTGATCTTCTGAAAAAGCAAATTGATTGTTCCCAGTGACA
A S V A R Y S D L P E K A N *
      790     800     810     820     830     840
CCAGACTGCTGTCAGCTTTTGGTTAAAGCCCGAAAGACAAAAGGACATTTGTAGTTTAGT
      850     860     870     880     890     900
TTATATTTCCCTTTCATTTGTGAATCAACATTGTACTCTCTGTAAACCTTTAAATGCTC
      910
CATTAACCT 3' (SEQ ID NOs: 27 & 28)
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